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SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Cahoon, Edgar B.
Cahoon, Rebecca E.
Kinney, Anthony J.
Rafalski, J. Antoni

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<141> 2002-10-30

<150> 60/083,688

<151> 1988-04-30

<150> PCT/US99/09280

<151> 1999-04-29

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      20                      25                      30
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His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
      35                      40                      45
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Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
50 55 60

Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser
65 70 75 80

Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu
85 90 95

Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr
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Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys
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Asp Tyr Val Tyr Lys Asp Met Ile Asp Phe Leu Asn Arg Phe Asn
130 135 140

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Glu Ser Arg Pro Pro Val Tyr Asp Leu Ser Lys Ile Pro Leu Asp Ile
35 40 45

Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys
50 55 60

Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys
65 70 75 80

Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile
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Gly Val Thr Ala Lys Asp Ile Val Tyr Asn Gln Ile Val Thr Phe Phe
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Arg Asn Gln Ala
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20 25 30

Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser
35 40 45

Thr Ala Val Thr Val His Gly Tyr Lys Cys Gln Glu Phe Glu Val Thr
50 55 60

Thr Asp Asp Gly Tyr Ile Leu Ser Val Gln Arg Ile Leu Glu Gly Arg
65 70 75 80

Ala Gly Gly Gly Gly Pro Lys Arg Pro Pro Val Leu Leu Gln His Gly
85 90 95

Val Leu Val Asp Gly Met Thr Trp Leu Val Asn Gly Pro Glu Gln Ser
100 105 110

Leu Ala Met Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ser Asn
115 120 125

Ile Arg Gly Thr Arg Phe Ser Arg Arg His Val Ser Leu Asp Pro Thr
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Asp Pro Glu Tyr Trp Asp Trp Ala Trp Asp Asp Leu Gly
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<213> Zea mays

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Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg
35 40 45
Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro
50 55 60
Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu
65 70 75 80
Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro
85 90 95
Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe
100 105 110
Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly
115 120 125
Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly
130 135 140
His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp
145 150 155 160
Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr
165 170 175
Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr
180 185 190
Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile
195 200 205
Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser
210 215 220
Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu
225 230 235 240

Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val
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Gln Ile Leu Asp Ser Leu Cys Asp Asp Glu His Leu Asp Cys Asn Asp
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 Ala Cys Cys Leu Met Asn Leu Gln Ser Val Leu Ser Ser Ser Arg Met
 20 25 30
 Arg Asn Thr Thr Asn Asp Ile Ser Asp Asp Lys Cys Pro Pro Gln Pro
 35 40 45

His Pro Leu Xaa Met Cys Arg Ser Arg Val Ala Ala Tyr Gly Tyr Pro
50 55 60

Cys Glu Glu Tyr His Val Thr Thr Glu Asp Gly Tyr Ile Leu Ser Leu
65 70 75 80

Lys Lys Ile Pro Tyr Gly Leu Ser Gly Xaa Thr Xaa Ile Thr Arg Xaa
85 90 95

Pro Val Leu Leu Phe His Gly Leu Leu Val Asp Gly Phe Cys Trp Val
100 105 110

Leu Asn Thr Pro Lys Gln Ser Leu Gly Phe Thr Trp Leu
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 35 40 45
 Val Ala Leu Ala Ala Phe Ser Glu Gly Arg Val Val Ser Gln Leu Lys
 50 55 60
 Ser Ala Ala Leu Leu Thr Pro Val Ala Tyr Leu Xaa His Xaa Asn Xaa
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 Pro Asn Xaa Asn Pro Gly Trp Pro Xaa Arg
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Ala Ala Ala Leu Arg Arg Val Gly Ser Gly Ser Gly Gly Leu Cys Asp
      35                      40                      45

Gln Leu Leu Leu Pro Leu Gly Tyr Pro Cys Thr Glu His Asn Val Glu
      50                      55                      60

Thr Lys Asp Gly Phe Leu Leu Ser Leu Gln His Ile Pro His Gly Lys
      65                      70                      75                      80

Asn Lys Ala Ala Asp Ser Thr Gly Pro Pro Val Phe Leu Gln His Gly
      85                      90                      95

Leu Phe Gln Gly Gly Asp Thr Trp Phe Ile Asn Ser Ala Glu Gln Ser
      100                      105                      110

Leu Gly Tyr Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Gly Asn
      115                      120                      125

Val Arg Gly Thr Arg Trp Ser Lys Gly His Ser Thr Phe Ser Val His
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Asp Lys Leu Phe Trp Asp Trp Ser Trp Gln Glu Leu Ala Glu Tyr Asp
      145                      150                      155                      160

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 165 170 175
 Leu Tyr Val Gly His Ser Gln Gly Thr Ile Met Gly Leu Ala Ala Leu
 180 185 190
 Thr Met Pro Glu Ile Val Lys Met Ile Ser Ser Ala Ala Leu Leu Cys
 195 200 205
 Pro Ile Ser Tyr Leu Asp His Val Ser Ala Ser Phe Val Leu Arg Ala
 210 215 220
 Val Ala Met His Leu Asp Gln Met Leu Val Thr Met Gly Ile His Gln
 225 230 235 240
 Leu Asn Phe Arg Ser Asp Met Gly Val Gln Ile Val Asp Ser Leu Cys
 245 250 255
 Asp Gly Glu His Val Asp Cys Asn Asn Leu Leu Ser Ala Ile Thr Gly
 260 265 270
 Glu Asn Cys Cys Phe Asn Thr Ser Arg Ile Asp Tyr Tyr Leu Glu Tyr
 275 280 285
 Glu Pro His Pro Ser Ser Thr Lys Asn Leu His His Leu Phe Gln Met
 290 295 300
 Ile Arg Lys Gly Thr Phe Ala Lys Tyr Asp Tyr Gly Leu Leu Gly Asn
 305 310 315 320
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 325 330 335
 Ile Pro Glu Ser Leu Pro Ile Trp Met Gly Tyr Gly Gly Leu Asp Ala
 340 345 350
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 355 360 365
 Thr Pro Glu Leu Leu Tyr Ile Gly Asp Tyr Gly His Ile Asp Phe Val
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 cngccncggc ggccacgtcg gcgaccggct catccgtgcc agtaacnttc nccatactcg 360
 cccacgnccn acttcgtcan tcgggntttc tgcgc 395

<210> 16
 <211> 80
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (8)
 <223> ANY AMINO ACID

<220>
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 <222> (10)..(11)
 <223> ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (15)
 <223> ANY AMINO ACID

<220>
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 <222> (61)
 <223> ANY AMINO ACID

<400> 16
 Thr Ser Phe Thr Gly Lys Asn Xaa Cys Xaa Xaa Asn Ser Ala Xaa Asp
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 Ile Phe Leu Lys Tyr Glu Pro Gln Pro Thr Ser Thr Lys Thr Leu Ile
 20 25 30

His Leu Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
 35 40 45

Val Met Pro Asp Ala Asn Val Ala Arg Tyr Gly Gln Xaa Asp Pro Pro
 50 55 60

Ala Tyr Asp Met Ala Ala Ile Pro Ala Trp Phe Pro Ile Phe Leu Ser
 65 70 75 80

<210> 17
 <211> 1718
 <212> DNA
 <213> Glycine max

<400> 17
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 aatacattaa cacttcaatc ccacgctttc aatagataga tagagcattc attcatcacc 180
 aacatggctc ttctaggctt aatgagtttt gctgccttga cccttttctt ggtcctaaca 240
 actgtgcctc gtcaagcaca cgcttcaagc cgtggcaact taggcagaaa catcaaccct 300
 tcagtgtatg gcatatgtgc ctcttctgtc attgtgcatg gatacaagtg tcaagaacac 360
 gaggttacaa ctgatgatgg ttacattctg agcctgcaaa ggatcccaga aggtcgaggt 420
 aaaagcagtg ggagtgggac aaggaagcaa ccagtgggta tacaacatgg agttcttgta 480
 gatggtatga catggcttct aaaccaccca gagcaagatc tgccgttgat tttagctgat 540
 aatggatttg acgtgtggat tgcaaacaca agaggaacca gatatagtcg ccgacacatc 600
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 ttataaaaac tatgtttcca aaaaaaaaaa aaaaaaaa 1718

<210> 18
 <211> 410
 <212> PRT
 <213> Glycine max

<400> 18
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 20 25 30

Leu Gly Arg Asn Ile Asn Pro Ser Val Tyr Gly Ile Cys Ala Ser Ser
 35 40 45

Val Ile Val His Gly Tyr Lys Cys Gln Glu His Glu Val Thr Thr Asp
 50 55 60
 Asp, Gly Tyr Ile Leu Ser Leu Gln Arg Ile Pro Glu Gly Arg Gly Lys
 65 70 75 80
 Ser Ser Gly Ser Gly Thr Arg Lys Gln Pro Val Val Ile Gln His Gly
 85 90 95
 Val Leu Val Asp Gly Met Thr Trp Leu Leu Asn Pro Pro Glu Gln Asp
 100 105 110
 Leu Pro Leu Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ala Asn
 115 120 125
 Thr Arg Gly Thr Arg Tyr Ser Arg Arg His Ile Ser Leu Asp Pro Ser
 130 135 140
 Ser Gln Ala Tyr Trp Asn Trp Ser Trp Asp Glu Leu Val Ser Tyr Asp
 145 150 155 160
 Phe Pro Ala Val Phe Asn Tyr Val Phe Ser Gln Thr Gly Gln Lys Ile
 165 170 175
 Asn Tyr Val Gly His Ser Leu Gly Thr Leu Val Ala Leu Ala Ser Phe
 180 185 190
 Ser Glu Gly Lys Leu Val Thr Gln Leu Lys Ser Ala Ala Leu Leu Ser
 195 200 205
 Pro Ile Ala Tyr Leu Ser His Met Asn Thr Ala Leu Gly Val Val Ala
 210 215 220
 Pro Lys Ser Phe Val Gly Glu Ile Thr Thr Leu Phe Gly Leu Ala Glu
 225 230 235 240
 Phe Asn Pro Lys Gly Leu Ala Val Asp Ala Phe Leu Lys Ser Leu Cys
 245 250 255
 Ala His Pro Gly Ile Asp Cys Tyr Asp Leu Leu Thr Ala Leu Thr Gly
 260 265 270
 Lys Asn Cys Cys Leu Asn Ser Ser Thr Val Asp Leu Phe Leu Met Asn
 275 280 285
 Glu Pro Gln Ser Thr Ser Thr Lys Asn Met Val His Leu Ala Gln Thr
 290 295 300
 Val Arg Leu Gly Ala Leu Thr Lys Phe Asn Tyr Val Arg Pro Asp Tyr
 305 310 315 320
 Asn Ile Met His Tyr Gly Glu Ile Phe Pro Pro Ile Tyr Asn Leu Ser
 325 330 335
 Asn Ile Pro His Asp Leu Pro Leu Phe Ile Ser Tyr Gly Gly Arg Asp
 340 345 350
 Ala Leu Ser Asp Val Arg Asp Val Glu Asn Leu Leu Asp Lys Leu Lys
 355 360 365

Phe His Asp Glu Asn Lys Arg Ser Val Gln Phe Ile Gln Glu Tyr Ala
 370 375 380

His Ala Asp Tyr Ile Met Gly Phe Asn Ala Lys Asp Leu Val Tyr Asn
 385 390 395 400

Ala Val Leu Ser Phe Phe Asn His Gln Val
 405 410

<210> 19
 <211> 1438
 <212> DNA
 <213> Glycine max

<400> 19
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 ataactgtct ccatactctt gggaaatgga aaccccggtc agtgcttcga cggcggtagc 120
 caccaaaaac agcaacacag tttgtgtgaa gagctcatta tcccctacgg ttacccttgc 180
 tccgagcata cgattcaaac gaaggatggt ttcttggttag gtcttcaacg tgtctcttct 240
 tcttcttctc ttcggtcttcg gaaccatgga gatggaggcc ctccggttct gcttctgcat 300
 ggattattca tggcagggtga tgcattggtt ctaaatactc cggaacaatc acttggcttc 360
 atacttgcag atcatggttt tgatgttttg gtaggaaacg tgcgtggaac acgctggagc 420
 catggacata tatctttatt agagaagaaa aagcaatttt gggattggag ttggcaggaa 480
 ttagccctgt atgatgttgc ggaaatgatc aattacatta attcagtaac aaactcaaag 540
 atattttag tagggcattc acaggggaca attatatctt tggctgcctt cactcaacca 600
 gagatagtag aaaagggttga ggctgcagct cttctatctc caatatcata cttggatcat 660
 gtcagtgac ctcttgtagc tagaatggtt aagatgcaca ttgatgagat gattcttacc 720
 atgggcattc atcaactaaa cttcaaaaagc gaatgggggg ccagtctctt ggtttcctta 780
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 aacttgaacc accttttcca gatgatccgc aaagggtacct actccaagta tgattatgga 960
 aagctaaaaa atctgataga gtacggcaag ttcaatccac caaagttcga tcttagtcgc 1020
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 aactatggtc atgttgactt cattttaagc ttgcaagcaa aacaagatct ttatgacctt 1200
 atgattagtt ttttcaagtc atccggaaaa tttagtagta tgtaatgttt gcttccttcc 1260
 ggtatgatgg atgtaattac tgtaatggtc tacgggtcca tctattactg cacttactgt 1320
 aaagttgaaa tattaatatt ctgtggagtc caccttgatt ttctgtatgt atatatgatg 1380
 acagatatat aaagatcggc gtcgcatgac ctgtttctgc aaaaaaaaaa aaaaaaaaaa 1438

<210> 20
 <211> 405
 <212> PRT
 <213> Glycine max

<400> 20
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 Leu Leu Gly Asn Gly Asn Pro Val Gln Cys Phe Asp Gly Gly Ser His
 20 25 30
 Gln Lys Gln Gln His Ser Leu Cys Glu Glu Leu Ile Ile Pro Tyr Gly
 35 40 45
 Tyr Pro Cys Ser Glu His Thr Ile Gln Thr Lys Asp Gly Phe Leu Leu
 50 55 60
 Gly Leu Gln Arg Val Ser Ser Ser Ser Ser Leu Arg Leu Arg Asn His
 65 70 75 80

Gly Asp Gly Gly Pro Pro Val Leu Leu Leu His Gly Leu Phe Met Ala
 85 90 95
 Gly Asp Ala Trp Phe Leu Asn Thr Pro Glu Gln Ser Leu Gly Phe Ile
 100 105 110
 Leu Ala Asp His Gly Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr
 115 120 125
 Arg Trp Ser His Gly His Ile Ser Leu Leu Glu Lys Lys Lys Gln Phe
 130 135 140
 Trp Asp Trp Ser Trp Gln Glu Leu Ala Leu Tyr Asp Val Ala Glu Met
 145 150 155 160
 Ile Asn Tyr Ile Asn Ser Val Thr Asn Ser Lys Ile Phe Val Val Gly
 165 170 175
 His Ser Gln Gly Thr Ile Ile Ser Leu Ala Ala Phe Thr Gln Pro Glu
 180 185 190
 Ile Val Glu Lys Val Glu Ala Ala Ala Leu Leu Ser Pro Ile Ser Tyr
 195 200 205
 Leu Asp His Val Ser Ala Pro Leu Val Leu Arg Met Val Lys Met His
 210 215 220
 Ile Asp Glu Met Ile Leu Thr Met Gly Ile His Gln Leu Asn Phe Lys
 225 230 235 240
 Ser Glu Trp Gly Ala Ser Leu Leu Val Ser Leu Cys Asp Thr Arg Leu
 245 250 255
 Ser Cys Asn Asp Met Leu Ser Ser Ile Thr Gly Lys Asn Cys Cys Phe
 260 265 270
 Asn Glu Ser Arg Val Glu Phe Tyr Leu Glu Gln Glu Pro His Pro Ser
 275 280 285
 Ser Ser Lys Asn Leu Asn His Leu Phe Gln Met Ile Arg Lys Gly Thr
 290 295 300
 Tyr Ser Lys Tyr Asp Tyr Gly Lys Leu Lys Asn Leu Ile Glu Tyr Gly
 305 310 315 320
 Lys Phe Asn Pro Pro Lys Phe Asp Leu Ser Arg Ile Pro Lys Ser Leu
 325 330 335
 Pro Leu Trp Met Ala Tyr Gly Gly Asn Asp Ala Leu Ala Asp Ile Thr
 340 345 350
 Asp Phe Gln His Thr Leu Lys Glu Leu Pro Ser Pro Pro Glu Val Val
 355 360 365
 Tyr Leu Glu Asn Tyr Gly His Val Asp Phe Ile Leu Ser Leu Gln Ala
 370 375 380
 Lys Gln Asp Leu Tyr Asp Pro Met Ile Ser Phe Phe Lys Ser Ser Gly
 385 390 395 400

Lys Phe Ser Ser Met
405

<210> 21
<211> 737
<212> DNA
<213> Zea mays

<400> 21
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tccaagaac aatccgtgtg acccatcaga atgatattgt gccgcattta ccaccgtatt 180
attattacct aggtgaatgg acataccacc acttcgctag agaggtttgg cttcatgaga 240
gcatagatgg aaatgtagtt accagaaacg agacggtatg tgatgattct ggtgaagacc 300
cgacctgtag caggtcggtc tatgggatga gcgtagcaga tcatcttgag tactatgatg 360
tcacactaca tgctgattca agaggaacct gtcaattcgt gattggtgca gccaaccaag 420
tatacaacta cgttcgtgaa gttgatggat ccatacatct gtcaagatac ccgcaagaac 480
cacaagctct agaatctatg tgactttgta tgccacggaa tgcaccctg tacagtattt 540
ttcattttca ttttgtgtac agctcatgaa atgctgggag ctccctggagc tctccagagg 600
ataaggagag gctcaccttt ttaaatgtgc cccctttgct caagtgagaa tcgtgcatgt 660
aagctccata agattgtccg cacaattcaa tttgtgtata taaataatac tatgtgttac 720
taaaaaaaaa aaaaaaa 737

<210> 22
<211> 166
<212> PRT
<213> Zea mays

<400> 22
Thr Arg Phe Cys Ala Leu Asp Leu Ser Val Lys Phe Gly Ser Gln Glu
1 5 10 15
Val Glu Leu Met Thr Phe Gly Gln Pro Arg Ile Gly Asn Pro Ala Phe
20 25 30
Ala Val Tyr Phe Gly Glu Gln Val Pro Arg Thr Ile Arg Val Thr His
35 40 45
Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Tyr Tyr Leu Gly
50 55 60
Glu Trp Thr Tyr His His Phe Ala Arg Glu Val Trp Leu His Glu Ser
65 70 75 80
Ile Asp Gly Asn Val Val Thr Arg Asn Glu Thr Val Cys Asp Asp Ser
85 90 95
Gly Glu Asp Pro Thr Cys Ser Arg Ser Val Tyr Gly Met Ser Val Ala
100 105 110
Asp His Leu Glu Tyr Tyr Asp Val Thr Leu His Ala Asp Ser Arg Gly
115 120 125
Thr Cys Gln Phe Val Ile Gly Ala Ala Asn Gln Val Tyr Asn Tyr Val
130 135 140
Arg Glu Val Asp Gly Ser Ile Ile Leu Ser Arg Tyr Pro Gln Glu Pro
145 150 155 160

Gln Ala Leu Glu Ser Met
165

<210> 23
<211> 1434
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (226)
<223> n = A, C, G, or T

<220>
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<222> (315)
<223> n = A, C, G, or T

<220>
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<222> (1306)
<223> n = A, C, G, or T

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<222> (1349)
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<222> (1359)
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<220>
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<222> (1368)
<223> n = A, C, G, or T

<220>
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<222> (1373)
<223> n = A, C, G, or T

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 ttatctacaa ccatactctt gcaaagacgc ttgtggaata tgcattnagcg gtgtatatga 240
 cagatttaac cgctctgttt acgtggacat gctcaagatg caatgacttg actcaaggat 300
 tcgagatgag atccntaatt gttgatgtgg agaaactgct tgcaggcatt gttggtgtag 360
 atcatagtct gaattcgata attggtgcaa tcaggggaac tcaagagaac agtgtacaga 420
 attggataaa agacttgata tgggaagcagc ttgatcctaag tnatccaaac atgccaaatg 480
 caaaggtgca cagtggattt ttctcctcgt ataacaatac aattttgcgt ctactctatca 540
 caagtgtgtg gcacaaggca agaaagtcac atggagatat caatgtcata gtgacaggcc 600
 actcgatggg aggagctatg gcttcttttt gcgcgctcga tcttgctatg aagcttgagg 660
 gtggcagtggt gcaactcatg acttttgggc agcctcgtgt tggcaatgct gcattcgctt 720
 catacttcgc caaatatgta cccaacacaa ttcgagtgac acacgggcat gatattgtgc 780
 cacatttgcc accttatttc tctttcttcc cccagctgac ataccacat ttccaagag 840
 aggtatgggt ccaggattct gatggcaaca caactgaacg gatttgtgac gacagcggtg 900
 aagacccaga ttgttgacag tgcattctcca tgttcggctt gaggattcag gaccattcac 960

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ttacctagga gttgatatgg aagcggacga ctggagcacc tgtagaatca tcacagctca 1020
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gacgtctcca tcgttgaacc tagtgtacaa aacagattgg agcagttcta gataggcgga 1140
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aaaatcatag gacgtttatg ctgattggna ggattgctnt ggtaatanat gancatgtaa 1380
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<210> 24
 <211> 296
 <212> PRT
 <213> Zea mays

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 <222> (50)
 <223> ANY AMINO ACID

<220>
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 <222> (80)
 <223> ANY AMINO ACID

<220>
 <221> UNSURE
 <222> (129)
 <223> ANY AMINO ACID

<400> 24
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 Arg Ser Phe Ile Tyr Asn His Thr Leu Ala Lys Thr Leu Val Glu Tyr
 35 40 45
 Ala Xaa Ala Val Tyr Met Thr Asp Leu Thr Ala Leu Phe Thr Trp Thr
 50 55 60
 Cys Ser Arg Cys Asn Asp Leu Thr Gln Gly Phe Glu Met Arg Ser Xaa
 65 70 75 80
 Ile Val Asp Val Glu Lys Leu Leu Ala Gly Ile Val Gly Val Asp His
 85 90 95
 Ser Leu Asn Ser Ile Ile Val Ala Ile Arg Gly Thr Gln Glu Asn Ser
 100 105 110
 Val Gln Asn Trp Ile Lys Asp Leu Ile Trp Lys Gln Leu Asp Leu Ser
 115 120 125
 Xaa Pro Asn Met Pro Asn Ala Lys Val His Ser Gly Phe Phe Ser Ser
 130 135 140
 Tyr Asn Asn Thr Ile Leu Arg Leu Ala Ile Thr Ser Ala Val His Lys
 145 150 155 160

Ala Arg Lys Ser Tyr Gly Asp Ile Asn Val Ile Val Thr Gly His Ser
165 170 175

Met Gly Gly Ala Met Ala Ser Phe Cys Ala Leu Asp Leu Ala Met Lys
180 185 190

Leu Gly Gly Gly Ser Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val
195 200 205

Gly Asn Ala Ala Phe Ala Ser Tyr Phe Ala Lys Tyr Val Pro Asn Thr
210 215 220

Ile Arg Val Thr His Gly His Asp Ile Val Pro His Leu Pro Pro Tyr
225 230 235 240

Phe Ser Phe Leu Pro Gln Leu Thr Tyr His His Phe Pro Arg Glu Val
245 250 255

Trp Val Gln Asp Ser Asp Gly Asn Thr Thr Glu Arg Ile Cys Asp Asp
260 265 270

Ser Gly Glu Asp Pro Asp Cys Cys Arg Cys Ile Ser Met Phe Gly Leu
275 280 285

Arg Ile Gln Asp His Ser Leu Thr
290 295

<210> 25
<211> 1560
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (601)
<223> n = A, C, G, or T

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gcgtctccgc cgccgccgga tccggcgcgga tgactactac ttggacgtgg agagcggcag 180
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ttctccgtgt tcgaggtgag catgatggcc gccaaagatcg cctacgagaa cgccgcctac 300
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aacaagttcg tgggcgacca caccagcgag gcgttcgtgt tcaccgacaa ggcaagagga 420
cgcgagcgtg gtggtggtgt cgttcggggg caccgagccc ttcaacatgc gggactggtc 480
cacggacgta aacctgtcgt ggctgggcat gggcgagctg ggccacgtcc acgtcggctt 540
cctcaaggcg ctgggcctgc aggaggagga cggcaaggac gccacgcggg cgttcccaa 600
nggcgcccc aacgccgtcc cgggcaagcc gctggcctac tacgcgctgc gcgaggaggt 660
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cgccgcgctg gcgaccatct tcccggcgct gctggcgctt caccggggagc ggggcgtcct 780
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tcatcagtat tattattggt gttgttgaat atatgcatcc tctcctctct atatagaatt 1380
 atagatacat gaggcctggc cggcgcgcga cgttgctgaa cagttgaagc gcttcccaaa 1440
 aaaaaatgta tcaactgtga agcatatata tccatgcatg catgtgtgcc cgaaattttt 1500
 gtttttaaaa aaaaaaaaaa aaaaaaaaaac aaaaaaaaaa aaaaaacaaa aaaaaaaaaa 1560

<210> 26
 <211> 258
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (45)
 <223> ANY AMINO ACID

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 20 25 30
 Glu Glu Asp Gly Lys Asp Ala Thr Arg Ala Phe Pro Xaa Gly Ala Pro
 35 40 45
 Asn Ala Val Pro Gly Lys Pro Leu Ala Tyr Tyr Ala Leu Arg Glu Glu
 50 55 60
 Val Gln Lys Gln Leu Gln Lys His Pro Asn Ala Asn Val Val Val Thr
 65 70 75 80
 Gly His Ser Leu Gly Ala Ala Leu Ala Thr Ile Phe Pro Ala Leu Leu
 85 90 95
 Ala Phe His Gly Glu Arg Gly Val Leu Asp Arg Leu Leu Ser Val Val
 100 105 110
 Thr Tyr Gly Gln Pro Arg Val Gly Asp Lys Val Phe Ala Gly Tyr Val
 115 120 125
 Arg Ala Asn Val Pro Val Glu Pro Leu Arg Val Val Tyr Arg Tyr Asp
 130 135 140
 Val Val Pro Arg Val Pro Phe Asp Ala Pro Pro Val Ala Asp Phe Ala
 145 150 155 160
 His Gly Gly Thr Cys Val Tyr Phe Asp Gly Trp Tyr Lys Gly Arg Glu
 165 170 175
 Ile Ala Lys Gly Gly Asp Ala Pro Asn Lys Asn Tyr Phe Asp Pro Arg
 180 185 190
 Tyr Leu Leu Ser Met Tyr Gly Asn Ala Trp Gly Asp Leu Phe Lys Gly
 195 200 205
 Ala Phe Leu Trp Ala Lys Glu Gly Lys Asp Tyr Arg Glu Gly Ala Val
 210 215 220
 Ser Leu Leu Tyr Arg Ala Thr Gly Leu Leu Val Pro Gly Ile Ala Ser
 225 230 235 240

His Ser Pro Arg Asp Tyr Val Asn Ala Val Arg Leu Gly Ser Val Ala
245 250 255

Ser Ala

<210> 27
<211> 432
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (7)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (15)
<223> n = A, C, G, or T

<220>
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<222> (27)
<223> n = A, C, G, or T

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<222> (38)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (50)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (94)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (99)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (103)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (105)
<223> n = A, C, G, or T

<220>
<221> unsure

<222> (117)

<223> n = A, C, G, or T

<400> 27

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catagtnata atacnaacag ttgcggncat tgagattntt ggaaatctgn tcggtgggca 60
aggaagacat atggaaggct acctataaat gttntaggnt cantncgatg ggagggncct 120
tttagcatcg ttcttgtgcc cttgacctct cttgttaagt atggatcgca ggaagttaa 180
ctcatgactt ttggacagcc tcgggtaggc aatccttctt ttgctgcgta cttcagtgc 240
caagtcccgga gaacaatccg tgtgacccat cagaatgaca ttgtcccaca cttgccacca 300
tatttttgct accttggcga atggacatat caccacttct cgagagaggt ttggcttcat 360
gagaccatag taggaaatgt agttactagg aatgagacca tctgtgatgg atcaggcgag 420
gacccaacat gc 432
```

<210> 28

<211> 106

<212> PRT

<213> *Oryza sativa*

<400> 28

```
Gly Pro Phe Ser Ile Val Leu Val Pro Leu Thr Ser Leu Val Lys Tyr
  1                      5                      10                      15
```

```
Gly Ser Gln Glu Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val Gly
          20                      25                      30
```

```
Asn Pro Ser Phe Ala Ala Tyr Phe Ser Asp Gln Val Pro Arg Thr Ile
          35                      40                      45
```

```
Arg Val Thr His Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Phe
          50                      55                      60
```

```
Cys Tyr Leu Gly Glu Trp Thr Tyr His His Phe Ser Arg Glu Val Trp
          65                      70                      75                      80
```

```
Leu His Glu Thr Ile Val Gly Asn Val Val Thr Arg Asn Glu Thr Ile
          85                      90                      95
```

```
Cys Asp Gly Ser Gly Glu Asp Pro Thr Cys
          100                      105
```

<210> 29

<211> 1234

<212> DNA

<213> Glycine max

<400> 29

```
ccactggaag atggaattcg tgagattttt tgattgctgg gaatgatttt caagaaaagg 60
ccacaaccca agtcttgatt gttttggaca agcatgagaa ccgcgatact tatgtggtag 120
ctttccgagg aacggaaccc tttgatgcag atgcatgggt cactgacctt gacatctcat 180
ggtacgcatt cccggcattg gaaaaatgca tgggtggcttc atgaaagcct tagggctaca 240
gaaaaatgtg gggtggccta aggagattca aagggatgaa aatcttcccc cgttggccta 300
ctatgttatt agggacattc taaggaaagg tttgagttaa aatcctaata caaagtttat 360
cattacgggt catagtttgg gtggagcact cgcaatcttg taccctacga tcatgttctt 420
gcatgatgag aagttgctga ttgagagggt ggaagggatc tacacgtttg ggcaaccaag 480
agttggagat gaagcatatg cacagtatat gagacaaaaa ttgagggaaa attctatcag 540
gtattgcagg tttgtttatt gcaatgacat agttccgagg ttgccctatg atgataagga 600
cttgctcttc aagcactttg ggatctgcct tttctttaac aggcgctatg aactcaggat 660
tctcgaagaa gagccgaata agaactatct ctgcgcatgg tgtgtgatac ccatgatgtt 720
caatgctgtt ttggaactaa taaggagcct taccatagcg tacaaaaatg gacctacta 780
tagagaagga tggtttctct ttagtttcag gttggttggt ctgctgattc ctggcttacc 840
```



```

tgctcacggt ccacaagatt atattaattc cactcttctg ggatcaattg aaaaacattt 900
taaagcagat tgatgtgtcc gtatacatga tcattccata ccactacgta catgtgtatg 960
gtcatgcaga ctaaaattta cataatcaag atttttagtt ttagaaaaaa tggtaataac 1020
acttgattat gtatcatgtg aagaatagtt atgtatcata atgatcatga ataataatac 1080
agtttgtcgt cagtacgagt tattgtatag taattaataa gctaggttta aagttgtttc 1140
ctttggtgca tggatttatc attaatgaga tcaatgtgaa gtttgtttat ttcaaaaaaa 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

```

<210> 30

<211> 246

<212> PRT

<213> Glycine max

<400> 30

```

His Leu Met Val Arg Ile Pro Gly Ile Gly Lys Met His Gly Gly Phe
 1                5                10                15

Met Lys Ala Leu Gly Leu Gln Lys Asn Val Gly Trp Pro Lys Glu Ile
      20                25                30

Gln Arg Asp Glu Asn Leu Pro Pro Leu Ala Tyr Tyr Val Ile Arg Asp
      35                40                45

Ile Leu Arg Lys Gly Leu Ser Glu Asn Pro Asn Ala Lys Phe Ile Ile
      50                55                60

Thr Gly His Ser Leu Gly Gly Ala Leu Ala Ile Leu Tyr Pro Thr Ile
      65                70                75                80

Met Phe Leu His Asp Glu Lys Leu Leu Ile Glu Arg Leu Glu Gly Ile
      85                90                95

Tyr Thr Phe Gly Gln Pro Arg Val Gly Asp Glu Ala Tyr Ala Gln Tyr
      100                105                110

Met Arg Gln Lys Leu Arg Glu Asn Ser Ile Arg Tyr Cys Arg Phe Val
      115                120                125

Tyr Cys Asn Asp Ile Val Pro Arg Leu Pro Tyr Asp Asp Lys Asp Leu
      130                135                140

Leu Phe Lys His Phe Gly Ile Cys Leu Phe Phe Asn Arg Arg Tyr Glu
      145                150                155                160

Leu Arg Ile Leu Glu Glu Glu Pro Asn Lys Asn Tyr Phe Ser Pro Trp
      165                170                175

Cys Val Ile Pro Met Met Phe Asn Ala Val Leu Glu Leu Ile Arg Ser
      180                185                190

Phe Thr Ile Ala Tyr Lys Asn Gly Pro His Tyr Arg Glu Gly Trp Phe
      195                200                205

Leu Phe Ser Phe Arg Leu Val Gly Leu Leu Ile Pro Gly Leu Pro Ala
      210                215                220

His Gly Pro Gln Asp Tyr Ile Asn Ser Thr Leu Leu Gly Ser Ile Glu
      225                230                235                240

```

Lys His Phe Lys Ala Asp
245

<210> 31
<211> 490
<212> DNA
<213> Glycine max

<400> 31
gcacgaggag agatggccta aagaaattga aaccgatgag aaccgtccac gtgtctatta 60
ctccataagg gatttgctaa agaagtgttt gaatagaaat gataaagcaa agttttattct 120
tacgggtcat agtcttggtg gagcacttgc aattcttttt cccgctatgc taattttgca 180
tgctgagaca tttcttttgg aaaggcttga aggggtgtac acatttggac agcctagggt 240
tgagatgaa acatttgcta aatacatgga aaatcaattg aaacattatg gcattaagta 300
ttttagggtt gtttactgca acgatattgt tcctagggtg ccctttgatg aagatatcat 360
gaaatttgag cattttggga catgtcttta ttatgacagg agctatacat gcaaggta 420
tatataagta ttttaatttt ttgattcatg catatatctg tcattgtaat caactttttt 480
ttttctgggg 490

<210> 32
<211> 141
<212> PRT
<213> Glycine max

<400> 32
His Glu Glu Arg Trp Pro Lys Glu Ile Glu Thr Asp Glu Asn Arg Pro
1 5 10 15
Arg Val Tyr Tyr Ser Ile Arg Asp Leu Leu Lys Lys Cys Leu Asn Arg
20 25 30
Asn Asp Lys Ala Lys Phe Ile Leu Thr Gly His Ser Leu Gly Gly Ala
35 40 45
Leu Ala Ile Leu Phe Pro Ala Met Leu Ile Leu His Ala Glu Thr Phe
50 55 60
Leu Leu Glu Arg Leu Glu Gly Val Tyr Thr Phe Gly Gln Pro Arg Val
65 70 75 80
Gly Asp Glu Thr Phe Ala Lys Tyr Met Glu Asn Gln Leu Lys His Tyr
85 90 95
Gly Ile Lys Tyr Phe Arg Phe Val Tyr Cys Asn Asp Ile Val Pro Arg
100 105 110
Leu Pro Phe Asp Glu Asp Ile Met Lys Phe Glu His Phe Gly Thr Cys
115 120 125
Leu Tyr Tyr Asp Arg Ser Tyr Thr Cys Lys Val His Ile
130 135 140

<210> 33
<211> 774
<212> DNA
<213> Triticum aestivum

<400> 33
gcacgagaat attcccatca tgggtgacagg acattccatg ggagggggcca tggcttcggt 60
ttgtgcccctt gatcttattg tcaactatgg gttaaaggac gtgaccctgc tgacatttgg 120

gcaacctcgg attggtaatg ctgtgtttgc taccaccttt aagaaatact tgccaaacgc 180
aattcgagtt accaaccgac atgatattgt gcctcatcta cccccgtact accagtactt 240
cccacagaat acctaccatc atttcccacc agaggtttgg gttcataaca ttggactcga 300
tagcctacta taccgatcg agcacatctg tgatcattct ggagaaagac cccacttgca 360
gcaggccctt gggttgaaat agcgtccagg cccatacccc ctttcttggc tccagcatcc 420
atcccgagtc gcgcggatca tccagaatcg tcacggatga caatatgctc aggcacaaag 480
ttgcccctgt agacggtgtt attgtcttct cgaagcagcc tggtttatca gttggtcagc 540
tactcagtac acagtaaaca agctcaagat tacatggatt tattttgatg tttttttttg 600
ccaaagaaca atattcttgt tggcaatcaa agcactatct catgtatata tacgcgtgtg 660
atcctggctg gattaaatta tcctagctga ggggtgtatt ctgaaatgta caaacatatc 720
tatgctgatt aaaaaaaaaa aaaaaaatac ttgaggcggc cccgtaccaa aaat 774

<210> 34
<211> 126
<212> PRT
<213> Triticum aestivum

<400> 34
His Glu Asn Ile Pro Ile Met Val Thr Gly His Ser Met Gly Gly Ala
1 5 10 15
Met Ala Ser Phe Cys Ala Leu Asp Leu Ile Val Asn Tyr Gly Leu Lys
20 25 30
Asp Val Thr Leu Leu Thr Phe Gly Gln Pro Arg Ile Gly Asn Ala Val
35 40 45
Phe Ala Thr His Phe Lys Lys Tyr Leu Pro Asn Ala Ile Arg Val Thr
50 55 60
Asn Ala His Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Gln Tyr Phe
65 70 75 80
Pro Gln Asn Thr Tyr His His Phe Pro Pro Glu Val Trp Val His Asn
85 90 95
Ile Gly Leu Asp Ser Leu Leu Tyr Pro Ile Glu His Ile Cys Asp His
100 105 110
Ser Gly Glu Arg Pro His Leu Gln Gln Ala Leu Gly Trp Lys
115 120 125

<210> 35
<211> 398
<212> PRT
<213> Canis familiaris

<400> 35
Met Trp Leu Leu Leu Thr Ala Ala Ser Val Ile Ser Thr Leu Gly Thr
1 5 10 15
Thr His Gly Leu Phe Gly Lys Leu His Pro Thr Asn Pro Glu Val Thr
20 25 30
Met Asn Ile Ser Gln Met Ile Thr Tyr Trp Gly Tyr Pro Ala Glu Glu
35 40 45
Tyr Glu Val Val Thr Glu Asp Gly Tyr Ile Leu Gly Ile Asp Arg Ile
50 55 60

Pro	Tyr	Gly	Arg	Lys	Asn	Ser	Glu	Asn	Ile	Gly	Arg	Arg	Pro	Val	Ala	
65					70					75					80	
Phe	Leu	Gln	His	Gly	Leu	Leu	Ala	Ser	Ala	Thr	Asn	Trp	Ile	Ser	Asn	
				85					90					95		
Leu	Pro	Asn	Asn	Ser	Leu	Ala	Phe	Ile	Leu	Ala	Asp	Ala	Gly	Tyr	Asp	
			100					105					110			
Val	Trp	Leu	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp	Ala	Arg	Arg	Asn	Leu	
		115					120					125				
Tyr	Tyr	Ser	Pro	Asp	Ser	Val	Glu	Phe	Trp	Ala	Phe	Ser	Phe	Asp	Glu	
	130					135					140					
Met	Ala	Lys	Tyr	Asp	Leu	Pro	Ala	Thr	Ile	Asp	Phe	Ile	Leu	Lys	Lys	
145					150					155					160	
Thr	Gly	Gln	Asp	Lys	Leu	His	Tyr	Val	Gly	His	Ser	Gln	Gly	Thr	Thr	
				165					170					175		
Ile	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Asn	Pro	Lys	Leu	Ala	Lys	Arg	Ile	
			180					185					190			
Lys	Thr	Phe	Tyr	Ala	Leu	Ala	Pro	Val	Ala	Thr	Val	Lys	Tyr	Thr	Glu	
		195					200					205				
Thr	Leu	Leu	Asn	Lys	Leu	Met	Leu	Val	Pro	Ser	Phe	Leu	Phe	Lys	Leu	
	210					215					220					
Ile	Phe	Gly	Asn	Lys	Ile	Phe	Tyr	Pro	His	His	Phe	Phe	Asp	Gln	Phe	
225					230					235					240	
Leu	Ala	Thr	Glu	Val	Cys	Ser	Arg	Glu	Thr	Val	Asp	Leu	Leu	Cys	Ser	
				245					250					255		
Asn	Ala	Leu	Phe	Ile	Ile	Cys	Gly	Phe	Asp	Thr	Met	Asn	Leu	Asn	Met	
			260					265					270			
Ser	Arg	Leu	Asp	Val	Tyr	Leu	Ser	His	Asn	Pro	Ala	Gly	Thr	Ser	Val	
		275					280					285				
Gln	Asn	Val	Leu	His	Trp	Ser	Gln	Ala	Val	Lys	Ser	Gly	Lys	Phe	Gln	
	290					295					300					
Ala	Phe	Asp	Trp	Gly	Ser	Pro	Val	Gln	Asn	Met	Met	His	Tyr	His	Gln	
305					310					315					320	
Ser	Met	Pro	Pro	Tyr	Tyr	Asn	Leu	Thr	Asp	Met	His	Val	Pro	Ile	Ala	
				325					330					335		
Val	Trp	Asn	Gly	Gly	Asn	Asp	Leu	Leu	Ala	Asp	Pro	His	Asp	Val	Asp	
			340					345					350			
Leu	Leu	Leu	Ser	Lys	Leu	Pro	Asn	Leu	Ile	Tyr	His	Arg	Lys	Ile	Pro	
		355					360					365				
Pro	Tyr	Asn	His	Leu	Asp	Phe	Ile	Trp	Ala	Met	Asp	Ala	Pro	Gln	Ala	
	370					375					380					

Val Tyr Asn Glu Ile Val Ser Met Met Gly Thr Asp Asn Lys
 385 390 395

<210> 36

<211> 403

<212> PRT

<213> Caenorhabditis elegans

<400> 36

Met Trp Arg Phe Ala Val Phe Leu Ala Ala Phe Phe Val Gln Asp Val
 1 5 10 15

Val Gly Ser His Gly Asp Pro Glu Leu His Met Thr Thr Pro Gln Ile
 20 25 30

Ile Glu Arg Trp Gly Tyr Pro Ala Met Ile Tyr Thr Val Ala Thr Asp
 35 40 45

Asp Gly Tyr Ile Leu Glu Met His Arg Ile Pro Phe Gly Lys Thr Asn
 50 55 60

Val Thr Trp Pro Asn Gly Lys Arg Pro Val Val Phe Met Gln His Gly
 65 70 75 80

Leu Leu Cys Ala Ser Ser Asp Trp Val Val Asn Leu Pro Asp Gln Ser
 85 90 95

Ala Gly Phe Leu Phe Ala Asp Ala Gly Phe Asp Val Trp Leu Gly Asn
 100 105 110

Met Arg Gly Asn Thr Tyr Ser Met Lys His Lys Asp Leu Lys Pro Ser
 115 120 125

His Ser Ala Phe Trp Asp Trp Ser Trp Asp Glu Met Ala Thr Tyr Asp
 130 135 140

Leu Asn Ala Met Ile Asn His Val Leu Glu Val Thr Gly Gln Asp Ser
 145 150 155 160

Val Tyr Tyr Met Gly His Ser Gln Gly Thr Leu Thr Met Phe Ser His
 165 170 175

Leu Ser Lys Asp Asp Gly Ser Phe Ala Lys Lys Ile Lys Lys Phe Phe
 180 185 190

Ala Leu Ala Pro Ile Gly Ser Val Lys His Ile Lys Gly Phe Leu Ser
 195 200 205

Phe Phe Ala Asn Tyr Phe Ser Leu Glu Phe Asp Gly Trp Phe Asp Ile
 210 215 220

Phe Gly Ala Gly Glu Phe Leu Pro Asn Asn Trp Ala Met Lys Leu Ala
 225 230 235 240

Ala Lys Asp Ile Cys Gly Gly Leu Lys Val Glu Ala Asp Leu Cys Asp
 245 250 255

Asn Val Leu Phe Leu Ile Ala Gly Pro Glu Ser Asp Gln Trp Asn Gln
 260 265 270

Thr Arg Val Pro Val Tyr Ala Thr His Asp Pro Ala Gly Thr Ser Thr
 275 280 285
 Gln Asn Ile Val His Trp Met Gln Met Val His His Gly Gly Val Pro
 290 295 300
 Ala Tyr Asp Trp Gly Thr Lys Thr Asn Lys Lys Lys Tyr Gly Gln Ala
 305 310 315 320
 Asn Pro Pro Glu Tyr Asp Phe Thr Ala Ile Lys Gly Thr Lys Ile Tyr
 325 330 335
 Leu Tyr Trp Ser Asp Ala Asp Trp Leu Ala Asp Thr Pro Asp Val Pro
 340 345 350
 Asp Tyr Leu Leu Thr Arg Leu Asn Pro Ala Ile Val Ala Gln Asn Asn
 355 360 365
 His Leu Pro Asp Tyr Asn His Leu Asp Phe Thr Trp Gly Leu Arg Ala
 370 375 380
 Pro Asp Asp Ile Tyr Arg Pro Ala Ile Lys Leu Cys Thr Asp Asp Tyr
 385 390 395 400
 Leu Gly Lys